

AMENDMENT

In the Specification:

Please amend the specification at page 3, after the third full paragraph, as follows:

--BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: This figure shows an elution profile of a concentrate of a supernatant of a culture of *Thermomonospora fusca* DSM 43793. The black band indicates fractions that exhibit ester group-cleaving activity.

Figure 2: This figure shows another elution profile of a concentrate of a supernatant of a culture of *Thermomonospora fusca* DSM 43793. The black band indicates fractions that exhibit ester group-cleaving activity.

Figure 3: This figure shows the amino acid sequence of the ester group-cleaving enzyme (SEQ ID No: 1) and the alignment with triacylglycerol-lipase from *Streptomyces albus* G (SEQ ID No. 2) and with triacylglycerol-acyl hydrolase from *Streptomyces* sp. M11 (SEQ ID No. 3).

Figure 4: This figure shows the weight loss by degradation of several ester-group containing polymers by means of the ester group-cleaving enzyme according to the invention.

Figure 5: This figure shows a comparison of the ester-cleavage of a polymer film by the ester cleaving-enzyme according to the invention and a lipase of *Pseudomonas* sp.

Figure 6: This figure shows the specific activity of the enzyme according to the invention for different triglycerides.

Figure 7: This figure shows ester cleavages/min of different phthalic acid esters by means of the ester-cleaving enzyme according to the invention and the lipase of *Pseudomonas* sp.--

Please amend the specification at page 12, after the heading "Characterisation of the enzyme according to the invention":

--Figure 3 shows the amino acid sequence of the enzyme according to the invention and the alignment, for the purpose of sequence comparison, with triacylglycerol-lipase from *Streptomyces albus* G and with triacylglycerol-acylhydrolase from *Streptomyces* sp. M11. The multiple alignment was produced using the "PileUp" program (Wisconsin Package, Version 9.1, Genetics Computer Group, Madison, WI, USA). ~~Amino acids differing from one another at identical positions are shown shaded. The black rimmed box indicates a highly conserved amino~~

~~acid sequence from the region of the active centre of lipases.~~ The sequences of the two Streptomyces strains originate from the SP-TREMBL Databank (Release 7.0, 08/1998): Q56008 (Streptomyces sp. M11)(SEQ ID No: 3), Q59798 (Streptomyces albus G)(SEQ ID No: 2).--

Please amend the specification at page 13, first full paragraph:

--In order to determine the entire sequence, the enzyme was digested with trypsin and GluC. --

After page 15, and before the first page of claims, kindly replace the previously filed Sequence Listing with the enclosed pages entitled --Sequence Listing--.